

SEQUENCE LISTING

<110> FREY, Perry A.
RUZICKA, Frank J.

<120> DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE

<130> 032026/0476

<140> US 09/330,611

<141> 1999-06-11

<150> US 09/198,942

<151> 1998-11-24

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<170> PatentIn Ver. 2.0

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gaa cta aag aaa tac ata cca tta aca aaa gaa gaa gaa gaa gga gta	144
Glu Leu Lys Lys Tyr Ile Pro Leu Thr Lys Glu Glu Glu Glu Gly Val	
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gct caa tgt gta aaa tca tta aga atg gct att act cca tat tat cta	192
Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu	
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tca tta atc gat cct aac gat cct aat gat cca gta aga aaa caa gct	240
Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala	
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att cca aca gca tta gag ctt aac aaa gct gct gca gat ctt gaa gac	288
Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp	
85 90 95	
cca tta cat gaa gat aca gat tca cca gta cct gga tta act cac aga	336
Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg	
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tat cca gat aga gta tta tta tta ata act gat atg tgc tca atg tac	384
Tyr Pro Asp Arg Val Leu Leu Leu Ile Thr Asp Met Cys Ser Met Tyr	
115 120 125	
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Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser	
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Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro	
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His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro	
195 200 205	
caa aga ata act cca gaa ctt gta aat atg ctt aaa aaa tat cat cca	672
Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro	
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Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly	
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Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr	
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Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro	
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 65 70 75 80
 Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp
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 Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg
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 Tyr Pro Asp Arg Val Leu Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
 115 120 125
 Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser
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 Pro Gln Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu Val
 165 170 175
 Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro
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 His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro
 195 200 205
 Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro
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 Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu
 225 230 235 240
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 245 250 255
 Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met
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 Val Ser Lys Gly Ile Glu Ile Ile Glu Gly Leu Arg Gly His Thr Ser
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 Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly Gly
 325 330 335
 Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys
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 Val Ile Leu Arg Asn Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro
 355 360 365
 Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys
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 Leu Asn Ile Asp Ala Glu Glu Lys Leu Leu Ala Gly Arg Ser Ala Lys
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 aaa ggc aat ccg gac gat cct ctt ttg cgt cag gta ctt acc tcg caa 240
 Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln
 65 70 75 80
 gat gag ttt gtc atc gcg ccc gga ttc tcc acc gac cca ctg gaa gaa 288
 Asp Glu Phe Val Ile Ala Pro Gly Phe Ser Thr Asp Pro Leu Glu Glu
 85 90 95

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ctt	ttg	ctg	gtc	aaa	ggc	ggc	tgc	gcg	gta	aat	tgc	cgc	tat	tgc	ttc	384
Leu	Leu	Leu	Val	Lys	Gly	Gly	Cys	Ala	Val	Asn	Cys	Arg	Tyr	Cys	Phe	
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cgt	cgt	cac	ttc	ccc	tat	gcc	gaa	aat	cag	ggc	aac	aag	cgt	aac	tgg	432
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Leu	Arg	Asp	Val	Asn	Asp	Asn	Ala	Gln	Thr	Leu	Ala	Asn	Leu	Ser	Asn	
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 Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu
 50 55 60
 Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln
 65 70 75 80
 Asp Glu Phe Val Ile Ala Pro Gly Phe Ser Thr Asp Pro Leu Glu Glu
 85 90 95
 Gln His Ser Val Val Pro Gly Leu Leu His Lys Tyr His Asn Arg Ala
 100 105 110
 Leu Leu Leu Val Lys Gly Gly Cys Ala Val Asn Cys Arg Tyr Cys Phe
 115 120 125
 Arg Arg His Phe Pro Tyr Ala Glu Asn Gln Gly Asn Lys Arg Asn Trp
 130 135 140
 Gln Thr Ala Leu Glu Tyr Val Ala Ala His Pro Glu Leu Asp Glu Met
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 Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu Asp
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 Trp Leu Leu Thr Gln Leu Glu Ala Ile Pro His Ile Lys Arg Leu Arg
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 Leu Val Glu Cys Phe Ala Arg Ser Thr Leu Gln Ile Leu Leu Val Asn
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 His Ile Asn His Ala Asn Glu Val Asp Glu Thr Phe Arg Gln Ala Met
 225 230 235 240
 Ala Lys Leu Arg Arg Val Gly Val Thr Leu Leu Asn Gln Ser Val Leu
 245 250 255
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 260 265 270
 Ala Leu Phe Asp Ala Gly Val Met Pro Tyr Tyr Leu His Val Leu Asp
 275 280 285
 Lys Val Gln Gly Ala Ala His Phe Met Val Ser Asp Asp Glu Ala Arg
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Gln Ile Met Arg Glu Leu Leu Thr Leu Val Ser Gly Tyr Leu Val Pro
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Ala Trp Leu Ile Lys His Leu Glu Asn Ile Pro His Leu Gln Arg Leu	
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Arg Ile His Thr Arg Leu Pro Val Val Ile Pro Gln Arg Ile Thr Asp	
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gaa ttt tgc act tta tta gca gaa act cgt ttg caa aca gtt atg gtg	672
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Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala	
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Leu Leu Lys Gly Val Asn Asp Asp Ala Gln Ile Leu Lys Ile Leu Ser	
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Leu Glu Phe Val Gln Ala Glu Gly Phe Ser Thr Asp Pro Leu Glu Glu
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 Val Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu
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 Glu Phe Cys Thr Leu Leu Ala Glu Thr Arg Leu Gln Thr Val Met Val
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 Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala
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 Asp Lys Leu Phe Gln Thr Gly Ile Leu Pro Tyr Tyr Leu His Leu Leu
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Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr	
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Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met	
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Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala	
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Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn	
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Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu	
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gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata	576
Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile	
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Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu	
195 200 205	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat	672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His	
210 215 220	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa	720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu	
225 230 235 240	
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg	768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu	
245 250 255	

ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg	816
Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val	
260 265 270	
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac	864
Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr	
275 280 285	
tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg	912
Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr	
290 295 300	
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc	960
Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr	
305 310 315 320	
tcg ggc tat gct gtt cct acc ttt gtg gta gat gct ccg ggg ggt ggt	1008
Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly	
325 330 335	
ggt aag ata cct gta atg ccg aac tat gtt gta tct cag tcc cca cga	1056
Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg	
340 345 350	
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag	1104
His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu	
355 360 365	
ccg gag aat tat cat gag gag tgt gat tgt gag gac tgt cga gcc ggt	1152
Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly	
370 375 380	
aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct	1200
Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala	
385 390 395 400	
atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac	1248
Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn	
405 410 415	
tga	1251

<210> 8
 <211> 416
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 8
 Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu
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 Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
 20 25 30
 Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Gly
 35 40 45
 Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
 50 55 60
 Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
 65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
 85 90 95
 Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
 100 105 110
 Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
 115 120 125
 Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
 130 135 140
 Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
 145 150 155 160
 Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
 165 170 175
 Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
 180 185 190
 Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
 195 200 205
 Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
 210 215 220
 Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
 225 230 235 240
 Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
 245 250 255
 Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
 260 265 270
 Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
 275 280 285
 Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
 290 295 300
 Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr
 305 310 315 320
 Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly
 325 330 335
 Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
 340 345 350
 His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
 355 360 365
 Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
 370 375 380
 Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
 385 390 395 400
 Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn
 405 410 415

<210> 9
 <211> 1416
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 9
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 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
 1 5 10 15
 tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
 20 25 30
 ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
 35 40 45
 ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
 50 55 60
 ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
 65 70 75 80
 ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
 85 90 95
 cac aaa aca aaa tac gat ctg gaa gac ccg ctt cat gag gat gaa gat 336
 His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp
 100 105 110
 tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
 115 120 125
 ctt gtc acg aat caa tgt tcc atg tac tgc cgc tac tgc aca aga agg 432
 Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg
 130 135 140
 cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
 145 150 155 160
 gct gca att gct tat atc ccg gaa aca ccc gaa atc cgc gat tgt tta 528
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
 165 170 175
 att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576
 Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
 180 185 190
 att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc 624
 Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
 195 200 205

gga aca aga gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg	672
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu	
210 215 220	
tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt	720
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe	
225 230 235 240	
aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag	768
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys	
245 250 255	
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca	816
Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala	
260 265 270	
ggt att aat gat tgc gtt cca att atg aaa aag ctc atg cat gac ttg	864
Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu	
275 280 285	
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca	912
Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser	
290 295 300	
gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc	960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile	
305 310 315 320	
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt	1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe	
325 330 335	
gtc gtt gac gca cca ggc gga gga ggt aaa atc gcc ctg cag cca aac	1056
Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn	
340 345 350	
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa	1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu	
355 360 365	
ggt gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag	1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln	
370 375 380	
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag	1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys	
385 390 395 400	
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tgc ttt	1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe	
405 410 415	
aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca	1296
Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala	
420 425 430	
aat ccg gag cat gaa aca tta aaa gat ccg cgt gag aaa aga gat cag	1344
Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln	
435 440 445	
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act	1392
Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr	
450 455 460	

gaa tgc gga ggg gat tct tca tga
 Glu Cys Gly Gly Asp Ser Ser
 465 470

1416

<210> 10
 <211> 471
 <212> PRT
 <213> Bacillus subtilis

<400> 10

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
 1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
 20 25 30

Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
 35 40 45

Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
 50 55 60

Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
 65 70 75 80

Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
 85 90 95

His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp
 100 105 110

Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
 115 120 125

Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
 165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
 180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
 195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
 210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
 225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
 260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val Asp Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
450 455 460

Glu Cys Gly Gly Asp Ser Ser
465 470

<210> 11
<211> 1188
<212> DNA
<213> Deinococcus radiodurans

<220>
<221> CDS
<222> (1)..(1188)

<400> 11
tgg caa ggc gta ccc gac gag cag tgg tac gac tgg aaa tgg cag ctc 48
Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu
1 5 10 15

aag aac cgc atc aac agt gtg gag gag ttg cag gaa gtc ctg acc ctc 96
Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu
20 25 30

acc gag tcc gag tac cgg ggt gcg tcc gcc gag ggc att ttc cgc ctc 144
Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu
35 40 45

gac atc acg ccg tat ttc gcg tcc ctc atg gac ccc gaa gac ccc acc 192
Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr
50 55 60

tgc ccg gtg cgc cgt cag gtg att ccc acc gag gag gag ctc cag ccg Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Leu Gln Pro 65 70 75 80	240
ttc acc tcc atg atg gaa gac tct ctc gcg gag gat aag cac tcg ccc Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro 85 90 95	288
gtg ccg ggg ctg gtg cac cgc tac ccc gac cgc gtg ctg atg ctg gtc Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val 100 105 110	336
acg acc cag tgc gcg agc tac tgc cgc tac tgc acc cga agc cgc atc Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile 115 120 125	384
gtg ggc gac ccc acc gag acg ttc aat ccc gcc gag tat gag gcg cag Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln 130 135 140	432
ctc aac tac ctg cgc aac acc ccg cag gtg cgc gac gtg ctg ctt tcc Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser 145 150 155 160	480
ggc ggc gac ccg ctc aca ctc gcg ccg aag gtg ctg ggg cgc ctg ctt Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu 165 170 175	528
tcc gaa ctt cgt aaa atc gag cac atc gaa atc atc cgc atc ggc acc Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr 180 185 190	576
cgc gtg ccc gtg ttc atg ccc atg cgc gtg acc cag gaa ctg tgc gac Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp 195 200 205	624
acg ctc gcc gaa cac cat ccg ctg tgg atg aac att cac gtc aac cac Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His 210 215 220	672
ccc aag gaa atc acc ccc gaa gtg gcc gag gcg tgt gac cgt ctg acc Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr 225 230 235 240	720
cgc gcg ggc gtg ccg ctc ggc aac cag agc gtg ctg ctg cgc ggc gtg Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val 245 250 255	768
aac gac cac ccg gtc atc atg caa aag ctg ctg cgc gag ctc gtc aaa Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys 260 265 270	816
att cgg gtg cgc ccc tac tac atc tac cag tgc gac ctc gtg cac ggc Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly 275 280 285	864
gct ggg cac ctg cgc acc acg gtc agt aag ggt ctg gaa atc atg gaa Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu 290 295 300	912
tcg ctg cgc ggc cac acc tcc ggc tac agc gtg ccg acc tac gtg gtg Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val 305 310 315 320	960

gac gcg ccc ggc ggc ggc ggc aag att ccg gtg gcg ccc aac tac gtg 1008
 Asp Ala Pro Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val
 325 330 335
 ctc tcg cac agc cct gag aag ctg att ctg cgc aac ttc gag ggc tac 1056
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr
 340 345 350
 atc gcc gcc tac tcg gag ccc acc gat tac acc ggc ccc gac atg gcg 1104
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala
 355 360 365
 att cct gac gac tgg att cgc aag gaa ccc ggc cag acc ggc atc ttc 1152
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe
 370 375 380
 ggc ctg atg gaa ggc gag cgc att tcc atc gag ccg 1188
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro
 385 390 395

<210> 12
 <211> 396
 <212> PRT
 <213> Deinococcus radiodurans

<400> 12
 Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu
 1 5 10 15
 Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu
 20 25 30
 Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu
 35 40 45
 Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr
 50 55 60
 Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro
 65 70 75 80
 Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro
 85 90 95
 Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val
 100 105 110
 Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile
 115 120 125
 Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln
 130 135 140
 Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser
 145 150 155 160
 Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu
 165 170 175
 Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr
 180 185 190

Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp
 195 200 205
 Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His
 210 215 220
 Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr
 225 230 235 240
 Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val
 245 250 255
 Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys
 260 265 270
 Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly
 275 280 285
 Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu
 290 295 300
 Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val
 305 310 315 320
 Asp Ala Pro Gly Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val
 325 330 335
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr
 340 345 350
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala
 355 360 365
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe
 370 375 380
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro
 385 390 395

<210> 13
 <211> 1113
 <212> DNA
 <213> Aquifex aeolicus

<220>
 <221> CDS
 <222> (1)..(1110)

<400> 13
 atg cgt cgc ttt ttt gag aat gta ccg gaa aac ctc tgg agg agc tac 48
 Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr
 1 5 10 15
 gag tgg cag ata caa aac agg ata aaa act ctt aag gag ata aaa aag 96
 Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys
 20 25 30
 tac tta aaa ctc ctt ccc gag gag gaa gaa gga att aaa aga act caa 144
 Tyr Leu Lys Leu Leu Pro Glu Glu Glu Gly Ile Lys Arg Thr Gln
 35 40 45

ggg ctt tat ccc ttt gcg ata aca cct tac tac ctc tct tta ata aat	192
Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn	
50 55 60	
cca gag gac ccg aag gat cct ata aga ctt cag gca atc ccc cgc gtt	240
Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val	
65 70 75 80	
gta gaa gtt gat gaa aag gtt cag tct gcg gga gaa cca gac gct ctg	288
Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu	
85 90 95	
aaa gaa gaa gga gat att ccg ggt ctt aca cac agg tat ccc gac agg	336
Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg	
100 105 110	
gtt ctt tta aac gtc act acc ttt tgt gcg gtt tac tgc agg cac tgt	384
Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys	
115 120 125	
atg aga aag agg ata ttc tct cag ggt gag agg gca agg act aaa gag	432
Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu	
130 135 140	
gaa ata gac acg atg att gat tac ata aag aga cac gaa gag ata agg	480
Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg	
145 150 155 160	
gat gtc tta att tca ggt ggt gag cca ctt tcc ctt tcc ttg gaa aaa	528
Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys	
165 170 175	
ctt gaa tac tta ctc tca agg tta agg gaa ata aaa cac gtg gaa att	576
Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile	
180 185 190	
ata cgc ttt ggg acg agg ctt ccc gtt ctt gca ccc cag agg ttc ttt	624
Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe	
195 200 205	
aac gat aaa ctt ctg gac ata ctg gaa aaa tac tcc ccc ata tgg ata	672
Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile	
210 215 220	
aac act cac ttc aac cat ccg aat gag ata acc gag tac gcg gaa gaa	720
Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu	
225 230 235 240	
gcg gtg gac agg ctc ctg aga agg ggc att ccc gtg aac aac cag aca	768
Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr	
245 250 255	
gtc cta ctt aaa ggc gta aac gac gac cct gaa gtt atg cta aaa ctc	816
Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu	
260 265 270	
ttt aga aaa ctt tta agg ata aag gta aag ccc cag tac ctc ttt cac	864
Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His	
275 280 285	
tgç gac ccg ata aag gga gcg gtt cac ttt agg act acg ata gac aaa	912
Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys	
290 295 300	

gga ctt gaa ata atg aga tat ttg agg gga agg ctg agc ggt ttc ggg	960
Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly	
305 310 315 320	
ata ccc act tac gcg gtg gac ctc ccg gga ggg aaa ggt aag gtt cct	1008
Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro	
325 330 335	
ctt ctt ccc aac tac gta aag aaa agg aaa ggt aat aag ttc tgg ttt	1056
Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe	
340 345 350	
gaa agt ttc acg ggt gag gtc gta gaa tac gaa gta acg gaa gta tgg	1104
Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp	
355 360 365	
gaa cct tga	1113
Glu Pro	
370	

<210> 14
 <211> 370
 <212> PRT
 <213> Aquifex aeolicus

<400> 14

Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr	
1 5 10 15	
Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys	
20 25 30	
Tyr Leu Lys Leu Leu Pro Glu Glu Glu Gly Ile Lys Arg Thr Gln	
35 40 45	
Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn	
50 55 60	
Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val	
65 70 75 80	
Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu	
85 90 95	
Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg	
100 105 110	
Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys	
115 120 125	
Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu	
130 135 140	
Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg	
145 150 155 160	
Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys	
165 170 175	
Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile	
180 185 190	

Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe
195 200 205

Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile
210 215 220

Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu
225 230 235 240

Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr
245 250 255

Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu
260 265 270

Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His
275 280 285

Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys
290 295 300

Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly
305 310 315 320

Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro
325 330 335

Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe
340 345 350

Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp
355 360 365

Glu Pro
370

<210> 15
<211> 1065
<212> DNA
<213> Treponema pallidum

<220>
<221> CDS
<222> (1)..(1065)

<400> 15
atg tct atg gct gag tgt acc cgg gaa cag aga aag aga cga ggt gca 48
Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala
1 5 10 15

ggg cgt gct gat gag cat tgg cgg acg ttg agt cct gcc tct tgc gcg 96
Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala
20 25 30

gca gat gcg ctg acg gag cat att tct cca gcg tat gcg cat tta att 144
Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile
35 40 45

gca caa gcg cag ggc gcg gac gcg cag gcg ctg aaa cgt cag gtg tgc 192
Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys
50 55 60

ttt gcg cca cag gag cgt gtg gtg cat gct tgc gag tgt gcc gac cca	240
Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro	
65 70 75 80	
ttg ggt gag gac cgg tac tgc gtg aca ccc ttt ttg gtg cat cag tat	288
Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr	
85 90 95	
gcg aat cgt gtg ttg atg ttg gca aca gga cgt tgc ttt tca cac tgt	336
Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys	
100 105 110	
cgc tat tgt ttt cgc cgc ggt ttc atc gcc caa cgt gca ggg tgg atc	384
Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile	
115 120 125	
ccc aac gaa gag cgc gag aag att att acg tat ctt cgt gct acc cct	432
Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro	
130 135 140	
tcg gtg aag gaa atc ctg gtt tca ggt ggt gat cca ctc act ggt tct	480
Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser	
145 150 155 160	
ttt gca cag gtc aca tcg ctt ttc cgc gca ctg cgc agt gta gcg ccg	528
Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro	
165 170 175	
gat ttg att att cgt ctg tgc act cgc gca gtc acc ttt gct ccg cag	576
Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln	
180 185 190	
gcc ttt act ccc gag ctg att gcg ttt ctg cag gag atg aag ccg gtg	624
Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val	
195 200 205	
tgg ata att ccg cat att aat cac ccg gca gag ctc ggt tct acg cag	672
Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln	
210 215 220	
cgc gcg gtg ctc gag gcc tgc gta ggc gca ggc ctc cct gtg caa tcg	720
Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser	
225 230 235 240	
cag tcg gta ctg ttg cgc ggg gtg aac gat tcg gta gag acg ctg tgc	768
Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys	
245 250 255	
aca ctg ttt cac gcg ctc act tgt ctg ggg gtt aag ccg ggg tat cta	816
Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu	
260 265 270	
ttt cag ttg gat ttg gcg cct gga act ggg gat ttt cgt gtg cca ctt	864
Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu	
275 280 285	
tct gac acg cta gct ctg tgg cgc aca ttg aag gag cgc ctc tca ggg	912
Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly	
290 295 300	
ttg tcg ctt ccc acg ctt gcg gtg gac ttg cca ggg ggt gga gga aag	960
Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Gly Lys	
305 310 315 320	

ttt ccg ctt gtg gca ttg gcc ttg cag caa gat gtc acg tgg cat cag 1008
 Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln
 325 330 335

gaa cgc gag gcg ttc tcc gca cgc ggc atc gat ggc gcg tgg tac acg 1056
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr
 340 345 350

tac ccg ttc 1065
 Tyr Pro Phe
 355

<210> 16
 <211> 355
 <212> PRT
 <213> Treponema pallidum

<400> 16
 Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala
 1 5 10 15

Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala
 20 25 30

Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile
 35 40 45

Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys
 50 55 60

Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro
 65 70 75 80

Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr
 85 90 95

Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys
 100 105 110

Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile
 115 120 125

Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro
 130 135 140

Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser
 145 150 155 160

Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro
 165 170 175

Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln
 180 185 190

Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val
 195 200 205

Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln
 210 215 220

Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser
 225 230 235 240

Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys
 245 250 255
 Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu
 260 265 270
 Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu
 275 280 285
 Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly
 290 295 300
 Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Gly Lys
 305 310 315 320
 Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln
 325 330 335
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr
 340 345 350
 Tyr Pro Phe
 355

<210> 17
 <211> 6
 <212> PRT
 <213> Clostridium subterminale

<400> 17
 Lys Asp Val Ser Asp Ala
 1 5

<210> 18
 <211> 17
 <212> DNA
 <213> Clostridium subterminale

<220>
 <221> modified_base
 <222> (9)
 <223> n is inosine

<220>
 <221> modified_base
 <222> (12)
 <223> n is inosine

<400> 18
 aargaygtnw sngaygc

17

<210> 19
 <211> 6
 <212> PRT
 <213> Clostridium subterminale

<400> 19
 Gln Ser His Asp Lys Val
 1 5

<210> 20
 <211> 20
 <212> DNA
 <213> Clostridium subterminale

<220>
 <221> modified_base
 <222> (3)
 <223> n is inosine

<220>
 <221> modified_base
 <222> (15)
 <223> n is inosine

<400> 20
 atnacytttrt crtgnswytg

20

<210> 21
 <211> 48
 <212> PRT
 <213> Clostridium subterminale

<400> 21
 Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys Val Ile Leu Arg Asn
 1 5 10 15

Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro Ile Asn Tyr Thr Pro
 20 25 30

Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys Lys Val His Lys Val
 35 40 45

<210> 22
 <211> 15
 <212> PRT
 <213> Clostridium subterminale

<400> 22
 Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln
 1 5 10 15

<210> 23
 <211> 16
 <212> PRT
 <213> Clostridium subterminale

<400> 23
 Met Ile Asn Arg Arg Tyr Glu Leu Phe Lys Asp Val Ser Asp Ala Asp
 1 5 10 15

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 24
atcctaacga tcctaattgat cc 22

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 25
tggatgggta aagtgaagtg 19

<210> 26
<211> 500
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Probe

<400> 26
atcctaacga tcctaattgat ccagtaagaa aacaagctat tccaacagca ttagagctta 60
acaaagctgc tgcagatctt gaagacccat tacatgaaga tacagattca ccagtacctg 120
gattaactca cagatatcca gatagagtat tattattaat aactgatatg tgctcaatgt 180
actgcagaca ctgtacaaga agaagatttg caggacaaag cgatgactct atgccaatgg 240
aaagaataga taaagctata gattatatca gaaatactcc tcaaggttaga gacgtattat 300
tatcaggtgg agacgctctt ttagtatctg atgaaacatt agaatacatc atagctaaat 360
taagagaaat accacacggt gaaatagtaa gaatagggtc aagaactcca gttgttcttc 420
cacaaagaat aactccagaa cttgtaaata tgcttaaaaa atatcatcca gtatgggttaa 480
acactcactt taaccatcca 500

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 27
tacacatatg ataaatagaa gatatg 26

<210> 28
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 28
tagactcgag ttattcttga acgtgtctc 29

<210> 29
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 29
tacagaattc atgataaata gaagatatg 29

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 30
tagaaagctt ttattcttga acgtgtctc 29

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 31
tataggatcc gaccgtataa ttcacgcat tacacc 36

<210> 32
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 32
tagagaattc gattcagtca ggcgtcccat tatic 34